

BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (64 letters)

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BLASTN 2.2.18 (Mar-02-2008)

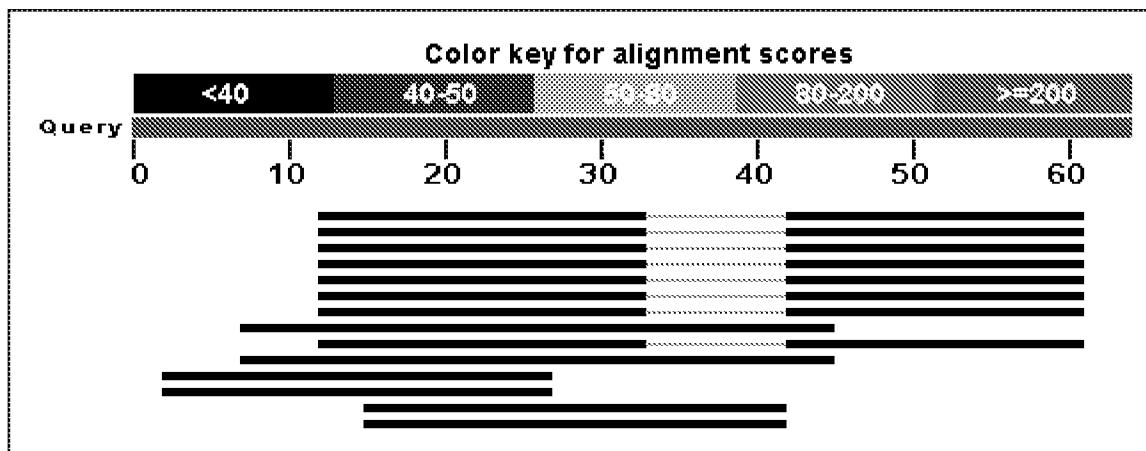
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 1HASZE0V012 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

Genome View

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= Length=64

Distribution of 22 Blast Hits on the Query Sequence















[Distance tree of results](#) [NEW](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure 

Sequences producing significant alignments:
(Click headers to sort columns)


Transcripts

NM_001080125.1	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant G, mRNA	39.2	74.7	62%	0.32	100%	 
NM_001080124.1	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant F, mRNA	39.2	74.7	62%	0.32	100%	 
NM_033358.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant E, mRNA	39.2	74.7	62%	0.32	100%	 
NM_033356.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant C, mRNA	39.2	74.7	62%	0.32	100%	 
NM_001228.4	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant A, mRNA	39.2	74.7	62%	0.32	100%	 
NM_033355.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant B, mRNA	39.2	74.7	62%	0.32	100%	 

Genomic sequences [show first]

NW_001838863.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188396)	39.2	74.7	62%	0.32	100%
NW_001839136.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188253)	39.2	39.2	59%	0.32	84%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	39.2	74.7	62%	0.32	100%
NT_008046.15	Homo sapiens chromosome 8 genomic contig, reference assembly	39.2	39.2	59%	0.32	84%
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	37.4	37.4	39%	1.1	92%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	37.4	37.4	39%	1.1	92%
NW_001842360.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188416)	35.6	35.6	42%	3.9	88%
NT_011757.15	Homo sapiens chromosome X genomic contig, reference assembly	35.6	35.6	42%	3.9	88%

Alignments

>ref|NM_001080125.1|  Homo sapiens caspase 8, apoptosis-related cysteine pe
(CASP8), transcript variant G, mRNA
Length=2938

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)


Sort alignments for this
E value Score Percen
Query start position

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query 13  AAGTTCCTGAGCCTGGACTAC 33
          |||||
Sbjct 445  AAGTTCCTGAGCCTGGACTAC 465
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 43  GTAGTCCAGGCTCAGGAAC 61
          |||||
Sbjct 465  GTAGTCCAGGCTCAGGAAC 447
```

>ref|NM_001080124.1|  Homo sapiens caspase 8, apoptosis-related cysteine pe
(CASP8), transcript variant F, mRNA
Length=2750

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)


Sort alignments for this
E value Score Percen
Query start position

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query 13  AAGTTCCTGAGCCTGGACTAC 33
          |||||
Sbjct 302  AAGTTCCTGAGCCTGGACTAC 322
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 43  GTAGTCCAGGCTCAGGAAC 61
          |||||
Sbjct 322  GTAGTCCAGGCTCAGGAAC 304
```

>ref|NM_033358.3|  Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant E, mRNA
Length=1123

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)


Sort alignments for this
E value Score Percen
Query start position

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query 13  AAGTTCCTGAGCCTGGACTAC 33
          |||
Sbjct 370  AAGTTCCTGAGCCTGGACTAC 390
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 43  GTAGTCCAGGCTCAGGAAC 61
          |||
Sbjct 390  GTAGTCCAGGCTCAGGAAC 372
```

>ref|NM_033356.3|  Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant C, mRNA
Length=2655

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)


Sort alignments for this
E value Score Percen
Query start position

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query 13  AAGTTCCTGAGCCTGGACTAC 33
          |||
Sbjct 207  AAGTTCCTGAGCCTGGACTAC 227
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 43  GTAGTCCAGGCTCAGGAAC 61
          |||
Sbjct 227  GTAGTCCAGGCTCAGGAAC 209
```

>ref|NM_001228.4|  Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant A, mRNA
Length=2914

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

Sort alignments for this
E value Score Percen
Query start position

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```

Query   13      AAGTTCCTGAGCCTGGACTAC   33
          |||||
Sbjct   370      AAGTTCCTGAGCCTGGACTAC   390


```

Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```

Query   43      GTAGTCCAGGCTCAGGAAC   61
          |||||
Sbjct   390      GTAGTCCAGGCTCAGGAAC   372

```

>ref|NM_033355.3|  Homo sapiens caspase 8, apoptosis-related cysteine pep
 (CASP8), transcript variant B, mRNA
 Length=2769

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
 [Homo sapiens] (Over 100 PubMed links)

Sort alignments for this
 E value Score Percen
 Query start position

Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```

Query   13      AAGTTCCTGAGCCTGGACTAC   33
          |||||
Sbjct   276      AAGTTCCTGAGCCTGGACTAC   296


```

Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```

Query   43      GTAGTCCAGGCTCAGGAAC   61
          |||||
Sbjct   296      GTAGTCCAGGCTCAGGAAC   278

```

>ref|NW_001838863.1|Hs2_WGA256_36  Homo sapiens chromosome 2 genomic contig, al
 (based on HuRef SCAF_1103279188396)
 Length=44081246

Sort alignments for this
 E value Score Percen
 Query start position

Features in this part of subject sequence:
 caspase 8 isoform G precursor
 caspase 8 isoform E

Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```


Query   13      AAGTTCCTGAGCCTGGACTAC   33
          |||||
Sbjct   27538620  AAGTTCCTGAGCCTGGACTAC   27538640

```

Features in this part of subject sequence:
 caspase 8 isoform G precursor
 caspase 8 isoform E

Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus


```
Query  43          GTAGTCCAGGCTCAGGAAC  61
                |||||
Sbjct  27538640    GTAGTCCAGGCTCAGGAAC  27538622
```

>ref|NW_001839136.1|Hs8_WGA529_36  Homo sapiens chromosome 8 genomic contig, al
 (based on HuRef SCAF_1103279188253)
 Length=44702525

Features in this part of subject sequence:
 hypothetical protein

Score = 39.2 bits (42), Expect = 0.32
 Identities = 32/38 (84%), Gaps = 1/38 (2%)
 Strand=Plus/Plus

```
Query  8          CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA  45
                ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  22623652    CCATAAAGTTACTGAGCCTGGA-TACTCTCCTAAATTA  22623688
```

>ref|NT_005403.16|Hs2_5560  Homo sapiens chromosome 2 genomic contig, reference
 Length=84213157

Sort alignments for this
 E value Score Perce
 Query start position

Features in this part of subject sequence:
 caspase 8 isoform G precursor
 caspase 8 isoform E


Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```
Query  13          AAGTTCCTGAGCCTGGACTAC  33
                |||||
Sbjct  52340693    AAGTTCCTGAGCCTGGACTAC  52340713
```

Features in this part of subject sequence:
 caspase 8 isoform G precursor
 caspase 8 isoform E

Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query  43          GTAGTCCAGGCTCAGGAAC  61
                |||||
Sbjct  52340713    GTAGTCCAGGCTCAGGAAC  52340695
```

>ref|NT_008046.15|Hs8_8203  Homo sapiens chromosome 8 genomic contig, reference
 Length=57155273

Features in this part of subject sequence:
 hypothetical protein

Score = 39.2 bits (42), Expect = 0.32
 Identities = 32/38 (84%), Gaps = 1/38 (2%)
 Strand=Plus/Plus

```
Query  8          CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA  45
```


Database: human build 36.3 reference assembly genomic scaffolds

Posted date: Apr 16, 2008 7:40 PM

Number of letters in database: 1,523,044,440

Number of sequences in database: 49,942

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.634	0.408	0.912

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 49942

Number of Hits to DB: 437151

Number of extensions: 24062

Number of successful extensions: 152

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 152

Number of HSP's successfully gapped: 0

Length of query: 64

Length of database: 5818011736

Length adjustment: 30

Effective length of query: 34

Effective length of database: 5816513476

Effective search space: 197761458184

Effective search space used: 197761458184

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 30 (28.3 bits)

S2: 37 (34.6 bits)